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☐ 1: NP_115972. ATP-binding casse...[gi:21729873]

Links

LOCUS ABCC11 1382 aa linear PRI 05-NOV-2002

DEFINITION ATP-binding cassette, sub-family C, member 11 isoform a;
multi-resistance protein 8; ATP-binding cassette transporter MRP8;
ATP-binding cassette protein C11 [Homo sapiens].

ACCESSION NP_115972

VERSION NP_115972.2 GI:21729873

DBSOURCE REFSEQ: accession NM_032583.2

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 1382)

AUTHORS Dean,M., Rzhetsky,A. and Allikmets,R.

TITLE The human ATP-binding cassette (ABC) transporter superfamily

JOURNAL Genome Res. 11 (7), 1156-1166 (2001)

MEDLINE 21329047

PUBMED 11435397

REFERENCE 2 (residues 1 to 1382)

AUTHORS Tammur,J., Prades,C., Arnould,I., Rzhetsky,A., Hutchinson,A.,
Adachi,M., Schuetz,J.D., Swoboda,K.J., Ptacek,L.J., Rosier,M.,
Dean,M. and Allikmets,R.

TITLE Two new genes from the human ATP-binding cassette transporter
superfamily, ABCC11 and ABCC12, tandemly duplicated on chromosome
16q12

JOURNAL Gene 273 (1), 89-96 (2001)

MEDLINE 21376129

PUBMED 11483364

REFERENCE 3 (residues 1 to 1382)

AUTHORS Bera,T.K., Lee,S., Salvatore,G., Lee,B. and Pastan,I.

TITLE MRP8, a new member of ABC transporter superfamily, identified by
EST database mining and gene prediction program, is highly
expressed in breast cancer

JOURNAL Mol. Med. 7 (8), 509-516 (2001)

MEDLINE 21475973

PUBMED 11591886

REFERENCE 4 (residues 1 to 1382)

AUTHORS Yabuuchi,H., Shimizu,H., Takayanagi,S. and Ishikawa,T.

TITLE Multiple splicing variants of two new human ATP-binding cassette
transporters, ABCC11 and ABCC12

JOURNAL Biochem. Biophys. Res. Commun. 288 (4), 933-939 (2001)

MEDLINE 21547789

PUBMED 11688999

COMMENT REVIEWED REFSEQ: This record has been curated by NCBI staff. The
reference sequence was derived from AF367202.1.
On Jul 11, 2002 this sequence version replaced gi:14211905.
Summary: The protein encoded by this gene is a member of the

superfamily of ATP-binding cassette (ABC) transporters. ABC proteins transport various molecules across extra- and intra-cellular membranes. ABC genes are divided into seven distinct subfamilies (ABC1, MDR/TAP, MRP, ALD, OABP, GCN20, White). This ABC full transporter is a member of the MRP subfamily which is involved in multi-drug resistance. It is expressed at low levels in all tissues, except kidney, spleen, and colon. This gene and family member ABCC12 are determined to be derived by duplication and are both localized to chromosome 16q12.1. Their chromosomal localization, potential function, and expression patterns identify them as candidates for paroxysmal kinesigenic choreoathetosis, a disorder characterized by attacks of involuntary movements and postures, chorea, and dystonia. Multiple alternatively spliced transcript variants have been described for this gene. Transcript Variant: This variant (1), as well as variant 2, encodes the predominant isoform (a).

FEATURES

source

Location/Qualifiers

1..1382

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="16"

/map="16q12.1"

Protein

1..1382

/product="ATP-binding cassette, sub-family C, member 11 isoform a"

/note="multi-resistance protein 8; ATP-binding cassette transporter MRP8; ATP-binding cassette protein C11"

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163..427

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/note="ABC_membrane"

/db_xref="CDD:pfam00664"

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536..691

/region_name="ATPases associated with a variety of cellular activities"

/note="AAA"

/db_xref="CDD:smart00382"

Region

537..708

/region_name="ABC transporter. ABC transporters for a large family of proteins responsible for translocation of a variety of compounds across biological membranes. ABC transporters are the largest family of proteins in many completely sequenced bacteria. ABC transporters are composed of two copies of this domain and two copies of a transmembrane domain pfam00664. These four domains may belong to a single polypeptide or belong in different polypeptide chains"

/note="ABC_tran"

/db_xref="CDD:pfam00005"

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/note="ABC_membrane"

/db_xref="CDD:pfam00664"

Region

1168..1360

/region_name="ATPases associated with a variety of

cellular activities"

/note="AAA"

/db_xref="CDD:smart00382"

Region

1169..1351

/region_name="ABC transporter. ABC transporters for a large family of proteins responsible for translocation of a variety of compounds across biological membranes. ABC transporters are the largest family of proteins in many completely sequenced bacteria. ABC transporters are composed of two copies of this domain and two copies of a transmembrane domain pfam00664. These four domains may belong to a single polypeptide or belong in different polypeptide chains"

/note="ABC_tran"

/db_xref="CDD:pfam00005"

CDS

1..1382

/gene="ABCC11"

/coded_by="NM_032583.2:79..4227"

/note="transporter"

/db_xref="LocusID:85320"

/db_xref="MIM:607040"

ORIGIN

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1381 lr
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//

Revised: July 5, 2002.

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Oct 31 2002 16:00:17

FASTA searches a protein or DNA sequence data bank
version 3.3t05 March 30, 2000
Please cite:
W.R. Pearson & D.J. Lipman PNAS (1988) 85:2444-2448

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>SEQ ID NO 23 human transporter
vs /tmp/fastadAADZaWfX library
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1382 residues in 1 sequences

FASTA (3.34 January 2000) function [optimized, BL50 matrix (15:-5)] ktup: 2
join: 40, opt: 28, gap-pen: -12/ -2, width: 16
Scan time: 0.050

The best scores are: opt

gi|21729873|ref|NP_115972.2| ATP-binding cassette (1382) 4838

>>gi|21729873|ref|NP_115972.2| ATP-binding cassette, sub (1382 aa)
initn: 7928 initl: 4838 opt: 4838
Smith-Waterman score: 7606; 88.061% identity in 1382 aa overlap (1-1219:1-1382)

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| | | | | | | |
| gi 217 | MTRKRTYWVPNSSGGLVNRGIDIGDDMVSGLIYKTYTLQDGPWSQQERNPEAPGRAAVPP | | | | | |
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| | | | | | | |
| gi 217 | WGKYDAALRTMIPFRPKPRFPAPQPLDNAGLFSYLTVSWLTPLMIQSLRSRLDENTIPPL | | | | | |
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| | 130 | 140 | 150 | 160 | 170 | 180 |
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| gi 217 | SVHDASDKNVQRLHRLWEEEVSRRGIEKASVLLVMLRFQTRLIFDALLGICFCIASVLG | | | | | |
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| | 190 | 200 | 210 | 220 | 230 | 240 |
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| | | | | | | |
| gi 217 | PILIIPKILEYSEEQLGNVVHGVGLCFALFLSECVKSLSFSSSWIINQRTAIRFRAAVSS | | | | | |
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| | | | | | | |
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| | 370 | 380 | 390 | 400 | 410 | 420 |
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| | | | | | | |
| gi 217 | FAKIIEDLRRKERKLEKGLVQSLTSITLFIIPTVATAVWVLIHTSLKCLKLTASMAFSM | | | | | |
| | 370 | 380 | 390 | 400 | 410 | 420 |

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490 500 510 520 530 540
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490 500 510 520 530 540

550 560 570 580 590 600
SEQ GVCGNTGSGKSSLLSAILEEMHLLGSGVGVQGSLAYVPQAWIVSGNIRENILMGGAYDK
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1219 residues in 1 query sequences

1382 residues in 1 library sequences

Scomplib [version 3.3t05 March 30, 2000]

start: Mon-Nov 11 10:23:05 2002 done: Mon Nov 11 10:23:06 2002

Scan time: 0.050 Display time: 2.400

Function used was FASTA